

Crisper-X Import Specie

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Chapter 1

Deprecated List

Global [_tos](#) (char *str)

Useless

Chapter 2

File Index

2.1 File List

Here is a list of all documented files with brief descriptions:

main.cpp	Crisper-X Import Specie	5
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Chapter 3

File Documentation

3.1 main.cpp File Reference

Crisper-X Import Specie.

```
#include <stdio.h>
#include <stdlib.h>
#include <string.h>
#include "mysql.h"
#include "cJSON/cJSON.h"
```

Macros

- #define `LEN` 20
Max sgRNA length.
- #define `GENE_LEN` 8000000
Max gene sequence length.
- #define `PAM_LEN` 20
Max PAM length.

Functions

- int `check_pam` (const char *`str`, const char *`pam`)
Check if a PAM matches requested PAM.
- char `dna_rev_char` (char `ch`)
Convert nucleobase character.
- char * `dna_rev` (char *`sr`, const char *`s`, int `len`)
Get another DNA chain.
- int `readLine` (FILE *`file`)
Read a line from file.
- char * `_tos` (char *`str`)
- void `get_pam_info` (char `pam_id`[], const char `pam`[])
Get PAM ID from database using PAM nama.
- void `add` (char *`str`)
Add an row to database.
- void `finish` ()
Query all unsaved addings.

- int [getFileID](#) (const char *user_ID, const char *fileName)
Get PAM ID from database using PAM nama.
- int [main](#) (int args, char *argv[])
Main function.

Variables

- char [str](#) [[GENE_LEN](#)]
Gene swquence.
- char [buffer](#) [9182]
Buffer memory for all usage.
- MYSQL * [my_conn](#)
Mysql database connector.
- MYSQL_RES * [result](#)
Mysql result.
- MYSQL_ROW [sql_row](#)
Mysql row.
- int [sum](#) =0
Counter for addings in memory.
- char [sql](#) [500000] =""
Buffer memory for sql statement.

3.1.1 Detailed Description

Crisper-X Import Specie.

Author

Yi Zhao

Definition in file [main.cpp](#).

3.1.2 Function Documentation

3.1.2.1 char* [_tos](#) (char * [str](#))

Deprecated Useless

Definition at line 77 of file main.cpp.

3.1.2.2 void [add](#) (char * [str](#))

Add an row to database.

System will not querey the sql immediately, but save to memory to query simultaneous.

Definition at line 115 of file main.cpp.

3.1.2.3 int [check_pam](#) (const char * [str](#), const char * [pam](#))

Check if a PAM matches requested PAM.

R=A,G; M=A,C; W=A,T; S=C,G; K=G,T; Y=C,T; H=A,C,T; V=A,C,G; B=C,G,T; D=A,G,T; N=A,G,C,T.

Definition at line 23 of file main.cpp.

3.1.2.4 `char* dna_rev (char * sr, const char * s, int len)`

Get another DNA chain.

Reverse sequence and convert nucleobase character.

Definition at line 56 of file main.cpp.

3.1.2.5 `char dna_rev_char (char ch)`

Convert nucleobase character.

A–T and C–G.

Definition at line 45 of file main.cpp.

3.1.2.6 `void get_pam_info (char pam_id[], const char pam[])`

Get PAM ID from database using PAM nama.

Parameters

<i>pam_id</i>	PAM ID, an integer in string style.
<i>pam</i>	PAM name.

Definition at line 96 of file main.cpp.

3.1.2.7 `int getFileID (const char * user_ID, const char * fileName)`

Get PAM ID from database using PAM nama.

Parameters

<i>user_ID</i>	User ID, should be integer in string style.
<i>fileName</i>	File name.

Returns

corresponding file ID.

Definition at line 155 of file main.cpp.

3.1.2.8 `int main (int args, char * argv[])`

Main function.

Include read files, finding sgRNAs and inserting database.

Definition at line 177 of file main.cpp.

3.1.3 Variable Documentation

3.1.3.1 `int sum =0`

Counter for addings in memory.

See also

[add](#)

Definition at line 108 of file main.cpp.